AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph beginning at page 28, line 30 as follows:

Flow Cytometric Analysis. Cells were seeded in 25 ml flasks in conditions as described above. Following treatment, trypsinization and cell counting, LNCaP cells ($1x10^6$) were suspended in 1 mL PBS and incubated with 0.2 mL 0.4% ~~Triton~~ Triton® X-100 for 5 min at R/T in the presence of 50 µL of propidium iodide solution (50 µg/mL) and 20 µL of ribonuclease (10 mg/mL). DNA content per cell was measured by flow cytometry using an FACScalibur® flow cytometer and CellQuest® software (Becton Dickinson, Franklin Lakes, N.J.). Statistical analysis was performed on 10,000 events per sample.

Please amend the paragraph beginning at page 30, line 29 as follows:

We searched the database of Serial Analysis of Gene Expression (SAGE) to determine the steady state mRNA levels of individual PLA_2 enzymes in prostate cancer. The cDNA libraries used for SAGE was PR317 normal prostate and PR317 prostate cancer, respectively ~~(Lash *et al.*, 2000, *Genome Res.* 10:1051-1060)~~, as both are derived from microdissected prostate tissues. We found that $sPLA_2$-IIA mRNA was 22 times higher in prostate cancer than normal prostate, whereas other members were either not expressed in the prostate libraries or unchanged in cancer. To verify the SAGE result and extend the expression analysis to androgen-independent prostate cancer (AIPC), we examined $sPLA_2$-IIA expression by immunohistochemistry in prostate cancer tissues from patients treated with androgen-ablation therapy for 3 months prior to radical prostatectomy. Cancer cells remaining in specimens following androgen-

ablation therapy are regarded as being closest to AIPC, although they are confined within the prostate. Cancer specimens from patients undergoing radical prostatectomy without androgen ablation therapy served as the control. Two antibodies were used for immunohistochemistry, and both showed the same expression pattern. In the control group, (N=50), there was weak and patchy staining in benign glands (FIGS. 1A and C.) adjacent to cancer cells and extensive staining in cancer cells (FIG. 1 C.). In the androgen-ablated group (N=25), benign glands lost their staining, whereas AIPC cells maintained $sPLA_2$-IIA expression (FIGS. 1 B and C). We also found that the extent of $sPLA_2$-IIA staining is positively correlated with the tumour grade and post-operative PSA level (data not shown). The chromosomal location of $sPLA_2$-IIA (1p35.1-36) was also found to overlap with a prostate cancer susceptibility locus CAPB (Gibbs *et al* (1999) Am. J. Hum. Genet. 64:776-787). No difference was found in immunohistochemical staining for $cPLA_2$-α between normal and cancer cells irrespective of androgen status (data not shown).